

It is not believed that extensions of time or fees for net addition of claims are required beyond those that may otherwise be provided for in documents accompanying this paper. However, if additional extensions of time are necessary to prevent abandonment of this application, then such extensions of time are hereby petitioned under 37 C.F.R. § 1.136(a), and any fees required therefor (including fees for net addition of claims) are hereby authorized to be charged to our Deposit Account No. 19-0036.

Amendments

In the Specification:

Please substitute the following paragraphs/sections for the pending paragraphs/sections.

Please delete pending paragraph [0087] and substitute therefor the following paragraph [0087]:

(D) A number of computer algorithms have been described for identification of peptides in a larger protein that may satisfy the requirements of peptide binding motifs for specific MHC class I or MHC class II molecules. Because of the extensive polymorphism of MHC molecules, different peptides will often bind to different MHC molecules. Tables 1-3 list C35 peptides predicted to be MHC binding peptides using three different algorithms. Specifically, Tables 1 and 5 list C35 HLA Class I and II epitopes predicted using the rules found at the SYFPEITHI website

([wysiwyg://35/http://134.2.96.221/scripts/hlaserver.dll/EpPredict.htm](http://35/http://134.2.96.221/scripts/hlaserver.dll/EpPredict.htm)) and are based on the book "MHC Ligands and Peptide Motifs" by Rammensee, H.G., Bachmann, J. and Stevanovic, S. (Chapman & Hall, New York 1997). Table 2 lists predicted MHC binding peptides derived from the C35 sequence using the NIH BIMAS program available on the web (http://bimas.dcrt.nih.gov/cgi-bin/molbio/ken_parker_comboform). Finally, Tables 3 and 6 list predicted C35 peptides identified by the Tepitope program, a program for prediction of peptides that may bind to multiple different MHC class II molecules. Using Tepitope, four C35 peptides were identified as likely candidates for binding to a variety of HLA class II molecules. These peptides are, in general, longer than those binding to HLA class I and more degenerate in terms of binding to multiple HLA class II molecules. Unless expressly noted otherwise, all peptide sequences listed in Tables 1-6 refer to C35 peptide sequences appearing in SEQ ID NO:2 at the amino acid positions noted. --

Please delete pending Table 4 entitled "Modifications that Enhance HLA Class I Binding" located on pages 139-175 directly following paragraph [0088] and substitute therefor the following Table 4 entitled "Modifications that Enhance HLA Class I Binding":

TABLE 4

Modifications that Enhance HLA Class I Binding

(Unless otherwise indicated, examples apply to peptides of 9 amino acids; for 10-mers the amino acid at position 5 is disregarded and the resultant 9-mer is evaluated (http://bimas.dcrt.nih.gov/cgi-bin/molbio/hla_coefficient)

viewing_page. The modifications listed below are provided by way of example based on current data in existing databases and are not intended in any way to be an inclusive list of all potential alterations of peptides binding all potential HLA molecules, both known and unknown to date.)

HLA A*0101

Any altered peptide that has S or T at position 2

Any altered peptide that has D or E at position 3

Any altered peptide that has P at position 4

Any altered peptide that has A, F, I, L, M, P, V, or Y at position 7

Any altered peptide that has F, K, R, or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E, F, G, H, K, M, N, P, Q, R, W, Y

P3: E, K, R, W

P4: K, R

P7: D, E, G, R

P9: D, E, P

HLA A*0201

Any altered peptide that has F, I, K, L, M, V, W, or Y at position 1

Any altered peptide that has I, L, M, Q, or V at anchor position 2

Any altered peptide that has F, L, M, W, or Y at position 3

Any altered peptide that has D or E at position 4

Any altered peptide that has F at position 5

Any altered peptide that has F, I, L, M, V, W or Y at auxiliary anchor position 6

Any altered peptide that has F, or W at position 7

Any altered peptide that has F, W, or Y at position 8

Any altered peptide that has I, L, T or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, H, P

P2: C, F, H, K, N, P, R, S, W, Y

P3: D, E, K, R

P7: D, E, G, R

P8: I, V

P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-A*0205

Any altered peptide that has F, I, K, L, M, V, W, or Y at position 1

Any altered peptide that has E, I, L, M, Q, or V at anchor position 2

Any altered peptide that has F, L, M, W, or Y at position 3

Any altered peptide that has D or E at position 4

Any altered peptide that has F, Y at position 5

Any altered peptide that has F, I, L, M, V, W or Y at auxiliary anchor position 6

Any altered peptide that has F, or W at position 7

Any altered peptide that has F, W, or Y at position 8

Any altered peptide that has I, L, T or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P

P2: C, D, F, G, H, K, N, P, R, S, W, Y

P3: D, E, K, R

P7: D, E, R

P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-A*03

Any altered peptide that has G or K at position 1

Any altered peptide that has I, L, M, Q, T or V at anchor position 2

Any altered peptide that has F, I, L, M, V, W, or Y at position 3

Any altered peptide that has E, G or P at position 4

Any altered peptide that has F, I, P, V, W, Y at position 5

Any altered peptide that has F, I, L, M, or V at position 6

Any altered peptide that has F, I, L, M, W, or Y at position 7

Any altered peptide that has F, I, K, L, Q or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P
P2: D, E, F, G, H, K, N, R, S, W, Y
P7: G, K, R
P9: D, E, G, H, N, P, Q, S, T

HLA-A*1101

Any altered peptide that has G, K or R at position 1
Any altered peptide that has I, L, M, Q, T, V, Y at anchor position 2
Any altered peptide that has F, I, L, M, V, W, Y at position 3
Any altered peptide that has F, I, L, M, W or Y at position 7
Any altered peptide that has K or R at anchor position 9
Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P
P2: D, E, G, H, K, N, R, S, W
P7: K, R
P9: C, D, E, G, N, P, Q, S, T

HLA-A24

Any altered peptide that has K or R at position 1
Any altered peptide that has F or Y at anchor position 2
Any altered peptide that has E, I, L, M, N, P, Q, or V at position 3
Any altered peptide that has D, E, or P at position 4
Any altered peptide that has I, L, or V at position 5
Any altered peptide that has F at position 6
Any altered peptide that has N or Q at position 7
Any altered peptide that has E or K at position 8
Any altered peptide that has F, I, L, or M at anchor position 9
Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, H, K, R
P9: D, E, G, H, K, P, Q, R

HLA-A*3101

Any altered peptide that has K or R at position 1
Any altered peptide that has F, I, L, M, Q, T, V, or Y at anchor position 2
Any altered peptide that has F, I, L, M, V W, or Y at position 3
Any altered peptide that has F, I, L, M, or V at position 6
Any altered peptide that has F, I, L, M, W, or Y at position 7
Any altered peptide that has K or R at anchor position 9
Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P
P2: D, E, G, H, K, N, R, S
P7: K, R
P9: C, G, N, P, Q, S, T

HLA-A*3302

Any altered peptide that has D or E at position 1
Any altered peptide that has I, L, M, S, V or Y at anchor position 2
Any altered peptide that has R at anchor position 9
Any altered peptide where deleterious residues at the following positions are replaced:

P1: K, P, R
P2: D, E, K, R
P9: D, E, F, G, N, P, W, Y

HLA-B7

Any altered peptide that has A at position 1
Any altered peptide that has A, P or V at anchor position 2
Any altered peptide that has M or R at position 3
Any altered peptide that has P at position 5
Any altered peptide that has R at position 6
Any altered peptide that has I, L, M or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, F, H, K, R, W, Y
P3: D, E
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B8

Any altered peptide that has D or E at position 1
Any altered peptide that has A, C, L, or P at anchor position 2
Any altered peptide that has K or R at position 3
Any altered peptide that has D or E at position 4
Any altered peptide that has K or R at position 5
Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: K, P, R
P2: D, E, F, G, H, K, Q, R, W, or Y
P3: D, E
P5: D, E
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B8 (8-mer peptides)

Any altered peptide that has D or E at position 1
Any altered peptide that has A, C, L, or P at anchor position 2
Any altered peptide that has K or R at position 3
Any altered peptide that has D or E at position 4
Any altered peptide that has K or R at position 5
Any altered peptide that has I, L, M, or V at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: K, P, R
P2: D, E, F, G, H, K, Q, R, W, or Y
P3: D, E
P5: D, E
P8: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B14

Any altered peptide that has D or E at position 1
Any altered peptide that has K or R at anchor position 2
Any altered peptide that has F, I, L, M, P, V, W, Y at position 3
Any altered peptide that has H or R at position 5
Any altered peptide that has I, L, M, R, or V at position 6
Any altered peptide that has T at position 7
Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, F, W, or Y
P3: E, R
P5: E, W, Y
P9: D, E, G, H, K, N, P, Q, R

HLA-B*2702

Any altered peptide that has K or R at position 1
Any altered peptide that has E, L, M, N, Q or R at anchor position 2
Any altered peptide that has F, W, or Y at position 3
Any altered peptide that has F, I, L, W or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P
P2: D, F, G, H, K, W, or Y
P7: K
P9: D, E, G, K, N, P, Q, R, S

HLA-B27*05 (8-mer peptides)

Any altered peptide that has K or R at position 1
Any altered peptide that has E, L, M, N, Q or R at anchor position 2
Any altered peptide that has F, W, or Y at position 3
Any altered peptide that has F, I, K, L, M, R, V or Y at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P
P2: D, F, G, H, K, W, or Y
P7: K
P9: D, E, G, K, N, P, Q, R, S

HLA-B*3501 (8-mer peptides)

Any altered peptide that has K or R at position 1
Any altered peptide that has A, P, or S at anchor position 2
Any altered peptide that has K or R at position 3
Any altered peptide that has D or E at position 4
Any altered peptide that has D or E at position 5
Any altered peptide that has F, I, L, M, V, W or Y at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, F, H, K, R, W, Y
P3: D, E
P8: D, E, F, G, H, K, P, Q, R

HLA-B*3701

Any altered peptide that has D or E at anchor position 2
Any altered peptide that has I or V at position 5
Any altered peptide that has F, L, or M at position 8
Any altered peptide that has F, I, L, M, V or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P9: D, E, G, H, K, P, Q, R

HLA-B*3801

Any altered peptide that has F, H, P, W or Y at anchor position 2
Any altered peptide that has D or E at position 3
Any altered peptide that has D, E, or G at position 4

Any altered peptide that has A, I, L, M, or V at position 5

Any altered peptide that has K or Y at position 8

Any altered peptide that has F, I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E, K, R

P3: K, R

P9: D, E, G, H, K, P, Q, R

HLA-B*3901 (8-mer peptides)

Any altered peptide that has H or R at anchor position 2

Any altered peptide that has D, E, F, I, L, M, V, W, or W at position 3

Any altered peptide that has D or E at position 4

Any altered peptide that has I, L, M, or V at position 6

Any altered peptide that has I, L, M or V at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E

P3: K, R

P6: D, E, K, R

P8: D, E, G, H, K, P, Q, R

HLA-B*3902

Any altered peptide that has K or Q at anchor position 2

Any altered peptide that has F, I, L, M, V, W, or Y at position 5

Any altered peptide that has F, L, or M at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E

P3: K, R

P9: D, E, G, H, K, P, Q, R

HLA-B40

Any altered peptide that has A or G at position 1
Any altered peptide that has D or E at anchor position 2
Any altered peptide that has A, F, I, L, M, V, W, or Y at position 3
Any altered peptide that has P at position 4
Any altered peptide that has P at position 5
Any altered peptide that has A, L, M, or W at anchor position 9
Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: F, H, I, K, L, M, Q, R, V, W, or Y
P3: D, E, K, R
P9: D, E, G, H, K, N, P, Q, R

HLA-B44*03

Any altered peptide that has A, D, or S at position 1
Any altered peptide that has D or E at anchor position 2
Any altered peptide that has A, I, L, M, or V at position 3
Any altered peptide that has F, I, or P at position 4
Any altered peptide that has A, K, or V at position 5
Any altered peptide that has A, L, T, or V at position 6
Any altered peptide that has F, K, or T at position 7
Any altered peptide that has K at position 8
Any altered peptide that has F, W or Y at anchor position 9
Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: F, H, I, K, L, M, Q, R, V, W, Y
P9: D, E, G, H, K, N, P, Q, R

HLA-B*5101 (8-mer peptides)

Any altered peptide that has D, E, F, I, L, M, V, or Y at position 1

Any altered peptide that has A, G or P at anchor position 2

Any altered peptide that has F, W or Y at position 3

Any altered peptide that has D, E, G, I, K, or V at position 4

Any altered peptide that has A, G, I, S, T, or V at position 5

Any altered peptide that has I, K, L, N, or Q at position 6

Any altered peptide that has D, K, Q, or R at position 7

Any altered peptide that has I, L, M, or V at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: K, P, R

P2: D, E, H, K

P8: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B*5102

Any altered peptide that has F or Y at position 1

Any altered peptide that has A, G, or P at anchor position 2

Any altered peptide that has F, I, L, V, W, or Y at position 3

Any altered peptide that has E, G, H, K, L, N, Q, R, or T at position 4

Any altered peptide that has G, N, Q, T, or V at position 5

Any altered peptide that has I, N, Q, or T at position 6

Any altered peptide that has E, K, Q, or R at position 7

Any altered peptide that has K, R, T, or Y at position 8

Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E, H, K, R

P3: D, E, K, R

P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B*5102 (8-mer peptides)

Any altered peptide that has F or Y at position 1
Any altered peptide that has A, G, or P at anchor position 2
Any altered peptide that has F, I, L, V, W, or Y at position 3
Any altered peptide that has E, G, H, K, L, V, W, or Y at position 4
Any altered peptide that has G, N, Q, T, V at position 5
Any altered peptide that has I, N, or Q at position 6
Any altered peptide that has Q, or R at position 7
Any altered peptide that has I, L, M, or V at position 8
Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, H, K, R
P3: D, E, K, R
P8: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B*5103

Any altered peptide that has D, T, or V at position 1
Any altered peptide that has A, G, or P at anchor position 2
Any altered peptide that has D, F, L, or Y at position 3
Any altered peptide that has E, G, L, N, Q, R, T, or V at position 4
Any altered peptide that has A, G, M, N, Q, R, K or V at position 5
Any altered peptide that has I, K, or T at position 6
Any altered peptide that has M or V at position 7
Any altered peptide that has I, L, M, or V at anchor position 9
Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, H, K, R
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B*5201 (8-mer peptides)

Any altered peptide that has I, L, M, or V at position 1
Any altered peptide that has G, P, or Q at anchor position 2
Any altered peptide that has D, F, I, L, P, W, or Y at position 3
Any altered peptide that has A, E, I, K, L, P, or V at position 4
Any altered peptide that has A, F, G, I, L, M, T or V at position 5
Any altered peptide that has K, L, N, S or T at position 6
Any altered peptide that has E, K, Q, or Y at position 7
Any altered peptide that has F, I, L, M, or V at anchor position 8
Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: H, K, R
P3: R
P8: D, E, G, H, K, N, P, Q, R, S

HLA-B*5801

Any altered peptide that has I, K, or R at position 1
Any altered peptide that has A, S, or T at anchor position 2
Any altered peptide that has D at position 3
Any altered peptide that has E, K, or P at position 4
Any altered peptide that has F, I, L, M, or V at position 5
Any altered peptide that has F, I, L, or V at position 6
Any altered peptide that has L, M, N, or Y at position 7
Any altered peptide that has K, N, R, or T at position 8
Any altered peptide that has F, W, or Y at anchor position 9
Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P
P2: D, E, F, H, I, K, L, M, N, Q, R, V, W, Y
P9: D, E, G, H, K, N, P, Q, R, S

HLA-B*60

Any altered peptide that has D or E at anchor position 2
Any altered peptide that has A, I, L, M, S, or V at position 3
Any altered peptide that has L, I, or V at position 5
Any altered peptide that has I, L, M, V, or Y at position 7
Any altered peptide that has K, Q, or R at position 8
Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: F, H, I, K, L, M, Q, R, V, W, Y
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B*61

Any altered peptide that has G or R at position 1
Any altered peptide that has D or E at anchor position 2
Any altered peptide that has A, F, I, L, M, T, V, W, or Y at position 3
Any altered peptide that has I at position 6
Any altered peptide that has Y at position 7
Any altered peptide that has A, I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: F, H, I, K, L, M, Q, R, V, W, Y
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B*61 (8-mer peptides)

Any altered peptide that has G or R at position 1
Any altered peptide that has D or E at anchor position 2
Any altered peptide that has A, F, I, L, M, T, V, W, or Y at position 3
Any altered peptide that has I at position 6
Any altered peptide that has Y at position 7

Any altered peptide that has A, I, L, M, or V at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: F, H, I, K, L, M, Q, R, V, W, Y

P8: D, E, F, G, H, K, N, P, Q, R, S, W, Y

HLA-B*62

Any altered peptide that has I at position 1

Any altered peptide that has I, L, Q at anchor position 2

Any altered peptide that has G, K, R at position 3

Any altered peptide that has D, E, G, or P at position 4

Any altered peptide that has F, G, I, L, or V at position 5

Any altered peptide that has I, L, T, V at position 6

Any altered peptide that has T, V, or Y at position 7

Any altered peptide that has F, W, Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E, F, H, K, N, R, S, W, Y

P3: D, E

P6: D, E, K, R

P9: D, E, G, H, K, N, P, Q, R, S

HLA-Cw0301

Any altered peptide that has A or R at anchor position 2

Any altered peptide that has F, I, L, M, V, or Y at position 3

Any altered peptide that has E, P, or R at position 4

Any altered peptide that has N at position 5

Any altered peptide that has F, M, or Y at position 6

Any altered peptide that has K, M, R, or S at position 7

Any altered peptide that has T at position 8

Any altered peptide that has F, I, L, M at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P3: D, K, R
P6: D, E, K, R
P9: D, E, G, H, K, N, P, Q, R, S,

HLA-Cw0401

Any altered peptide that has F, P, W, or Y at anchor position 2
Any altered peptide that has D, or H at position 3
Any altered peptide that has D or E at position 4
Any altered peptide that has A, H, M, R, or T at position 5
Any altered peptide that has I, L, M, or V at position 6
Any altered peptide that has A at position 7
Any altered peptide that has H, K, or S at position 8
Any altered peptide that has F, I, L, M, V or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P2: D, E, H, K, R
P9: D, E, G, H, K, N, P, Q, R, S

HLA-Cw0602

Any altered peptide that has F, I, K, or Y at position 1
Any altered peptide that has A, P, Q, or R at anchor position 2
Any altered peptide that has F, I, K, L, or M at position 5
Any altered peptide that has I, L, or V at position 6
Any altered peptide that has K, N, Q, or R at position 7
Any altered peptide that has I, L, M, V, or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P
P9: D, E, G, H, K, N, P, Q, R, S

Examples of predicted human Class I MHC binding peptides from the C35 aa sequence and how they might be changed to improve binding:

HLA-A*0101

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
1	77	KLENGGRPY	225.000	
2	16	EVEPGSGV	90.000	
3	29	YCEPCGFEA	45.000	
4	39	YLELASAVK	36.000	
5	2	SGEPGQTSV	2.250	G is deleterious at P2
example of improved peptide		STEPGQTSV	22.50	G replaced with T @ P2 SEQ ID NO:85
example of improved peptide		STEPGQISY	5625.00	V at P9 replaced with Y, P7 enhanced SEQ ID NO:86

HLA-A*0101 (10-mer peptides)

1	66	EIEINGQLVF	45.000	
2	16	EVEPGSGVRI	18.000	
3	29	YCEPCGFEAT	9.000	
4	26	VVEYCEPCGF	9.000	
5	52	GIEIESRLGG	2.250	
example of improved peptide		GTEPSRLGY	1125.000	replace I with T @P2 replace G with Y @P9 P5 enhanced with P SEQ ID NO:87

HLA-A*0201 (9-mer peptides)

1	9	SVAPPPEEV	2.982
2	104	KITNSRPPC	2.391
3	105	ITNSRPPCV	1.642
4	25	IVVEYCEPC	1.485
5	65	FEIEINGQL	1.018

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

example of improved peptide **FLIEINWYL** **16619.000** SEQ ID NO:88

HLA-A*0201 (10-mer peptides)

1	58	RLGGTGAFEI	60.510	
2	104	KITNSRPPCV	33.472	
3	65	FEIEINGQLV	25.506	
4	83	F P YEKDLIEA	4.502	P is deleterious at P2

example of improved peptide **FLYEKDLIEA** **689.606** **replace P with L @ P2** SEQ ID NO:89

example of improved peptide **FLYEKDLIEV** **9654.485** **replace A with V @ P9** SEQ ID NO:90

5 33 CGFEATYLEL 3.173

HLA-A*0205

1	65	FEIEINGQL	8.820	
2	25	IVVEYCEPC	3.060	
3	9	SVAPPPEEV	2.000	
4	104	KITNSRPPC	1.500	
5	81	GGFPYEKDL	1.260	G is deleterious at P2

example of improved peptide **GVFPYEKDL** **50.400** **replace G with V @ P2** SEQ ID NO:91

HLA-A*0205 (10-mer peptides)

1 33 CGEFATYLEL 6.300 G is deleterious at P2

example of improved peptide **CVEFATYLEL** **11.200** **replace G with V @ P2** SEQ ID NO:92

2	104	KITNSRPPCV	6.000	
3	65	FEIEINGQLV	2.520	
4	53	IEIESRLGGT	1.428	

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

5	83	FPYEKDLIEA	1.350	<i>P</i> is deleterious at P2
---	----	------------	-------	-------------------------------

example of improved peptide **FVYEKDLIEA 54.000** replace **P** with **V** @ P2 SEQ ID NO:93

HLA-A24

1	34	GFEATYLEL	33.000
---	----	-----------	--------

2	49	QYPGIEIES	11.550
---	----	-----------	--------

example of improved peptide **QYPGIEIEL 462.000** enhance **P9** SEQ ID NO:94

3	70	NGQLZFSKL	11.088
---	----	-----------	--------

4	38	TYLELASAV	10.800
---	----	-----------	--------

5	82	GFPYEKDLI	7.500
---	----	-----------	-------

HLA-A24 (10-mer peptides)

1	64	AFEIEINGQL	42.000
---	----	------------	--------

2	74	VFSKLENGGF	10.000
---	----	------------	--------

3	84	PYEKDLIEAI	9.000
---	----	------------	-------

4	69	INGQLVFSKL	7.392
---	----	------------	-------

example of improved peptide **IYGQLVFSKL 369.6** enhance **P2** SEQ ID NO:95

5	28	EYCEPCGFEA	6.600
---	----	------------	-------

HLA-A3

1	77	KLENGGFPY	36.000
---	----	-----------	--------

example of improved peptide **KLENGGFPK 180.000** enhance **P9** SEQ ID NO:96

2	39	YLELASAVK	20.000
---	----	-----------	--------

3	101	TLEKITNSR	6.000
---	-----	-----------	-------

4	61	GTGAFEIEI	0.540
---	----	-----------	-------

5	69	INGQLVFSK	0.360	<i>N</i> is deleterious @ P2
---	----	-----------	-------	------------------------------

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

example of improved peptide **ILGQLVFSK** **180.000** **replace N with L @ P2** SEQ ID NO:97

HLA-A3 (10-mer peptides)

1	68	EINGQLVFSK	8.100	
2	58	RLGGTGAFEI	2.700	
3	41	ELASAVKEQY	1.800	
4	78	LENGGFPLYEK	0.810	<i>E</i> is deleterious @ P2

example of improved peptide **LLNGGFPLYEK** **270.000** **replace E with L @ P2** SEQ ID NO:98

5 95 RASNGETLEK 0.400

HLA- A*1101

1	39	YLELASAVK	0.400	
2	69	INGQLVFSK	0.120	<i>N</i> is deleterious @ P2

example of improved peptide **IVGQLVFSK** **6.000** **replace N with V @ P2** SEQ ID NO:99

3	16	EVEPGSGVR	0.120	
4	101	TLEKITNSR	0.080	
5	61	GTGAFEIEI	0.060	

HLA-A*1101 (10-mer peptides)

1	95	RASNGETLEK	1.200	
2	38	TYLELASAVK	0.600	
3	68	EINGGLVFSK	0.360	
4	78	LENGGFPLYEK	0.120	<i>E</i> is deleterious @ P2

example of improved peptide **LVNGGFPLYEK** **4.000** **replace E with V @ P2** SEQ ID NO:100

5 100 ETLEKITNSR 0.090

Examples of predicted human Class I MHC binding peptides - c ntinued

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-A*3101

1	101	TLEKITNSR	2.000	
2	16	EVEPGSGVR	0.600	
3	50	YPGIEIESR	0.400	
4	87	KDLIEAIRR	0.240	<i>D is deleterious @ P2</i>

example of improved peptide KILIEAIRR **12.000** **replace D with I @ P2** SEQ ID NO:101

5	39	YLELASAVK	0.200	
---	----	-----------	-------	--

HLA-A*3302

1	16	EVEPGSGVR	45.000	
2	101	TLEKITNSR	9.000	
3	50	YPGIEIESR	3.000	
4	66	EIEINGQLV	1.500	
5	56	ESRLGGTGA	1.500	

HLA-A*3302 (10-mer peptides)

1	49	QYPGIEIESR	15.000	
2	100	ETLEKITNSR	9.000	
3	16	EVEPGSGVRI	1.500	
4	28	EYCEPCGFEA	1.500	
5	68	EINGQLVFSK	1.500	

HLA-A68.1

1	16	EVEPGSGVR	900.000	
2	9	SVAPPPEEV	12.000	
3	50	YPGIEIESR	10.000	

example of improved peptide YVGIEIESR **400.000** **enhance P2** SEQ ID NO:102

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

4	96	ASNGETLEK	9.000	
---	----	-----------	-------	--

5	101	TLEKITNSR	5.000	
---	-----	-----------	-------	--

HLA-A68.1 (10-mer peptides)

1	100	ETLEKITNSR	300.000	
---	-----	------------	---------	--

2	16	EVEPGSGVRI	18.000	
---	----	------------	--------	--

3	68	EINGGLVFSK	9.000	
---	----	------------	-------	--

4	15	EEVEPGSGVR	9.000	<i>E is deleterious @ P2</i>
---	----	------------	-------	------------------------------

example of improved peptide		EVVEPGSGR	1200.00	replace E with V @ P2	SEQ ID NO:103
-----------------------------	--	-----------	---------	------------------------------	---------------

5	95	RASNGETLEK	3.000	
---	----	------------	-------	--

HLA-B14

1	94	RRASNGETL	20.000	
---	----	-----------	--------	--

2	57	SRLGGTGAF	5.000	
---	----	-----------	-------	--

example of improved peptide		SRLGGTGAL	100.000	enhance P9	SEQ ID NO:104
-----------------------------	--	-----------	---------	-------------------	---------------

3	100	ETLEKITNS	3.375	
---	-----	-----------	-------	--

4	105	ITNSRPPCV	2.000	
---	-----	-----------	-------	--

5	88	DLIEAIRRA	1.350	
---	----	-----------	-------	--

HLA-B14 (10-mer peptides)

1	103	EKITNSRPPC	6.750	
---	-----	------------	-------	--

example of improved peptide		ERITNSRPLL	900.000	enhance P10	SEQ ID NO:105
-----------------------------	--	------------	---------	--------------------	---------------

2	33	CGFEATYLEL	5.000	
---	----	------------	-------	--

3	93	IRRASNGETL	4.000	
---	----	------------	-------	--

4	18	EPGSGVRIVV	3.000	
---	----	------------	-------	--

5	88	DLIEAIRRAS	2.250	
---	----	------------	-------	--

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-B40

1	65	FEIEINGQL	80.000
2	3	GEPGQTSVA	40.000
3	35	FEATYLELA	40.000
4	15	EEVEPGSGV	24.000

example of improved peptide EEVEPGSGL **120.000** **enhance P9** SEQ ID NO:106

5	67	IEINGQLVF	16.000
---	----	-----------	--------

HLA-B40 (10-mer peptides)

1	55	IESRLGGTGA	20.000
2	53	IEIESRLGGT	16.000

example of improved peptide IEIESRLGGL **80.000** **enhance P10** SEQ ID NO:107

3	65	FEIEINGQLV	16.000
4	67	IEINGQLVFS	16.000
5	99	GETLEKITNS	8.000

HLA-B60

1	65	FEIEFNGQL	387.200
2	17	VEPGSGVRI	17.600

example of improved peptide VEPGSGVRL **352.000** **enhance P9** SEQ ID NO:108

3	15	EEVEPGSGV	16.000
4	47	KEQYPGIEI	16.000
5	85	YEKDLIEAI	8.800

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-B60 (10-mer peptides)

1	65	FEIEINGQLV	16.000
---	----	------------	--------

example of improved peptide **FEIEINGQLL** **320.000** **enhance P10** SEQ ID NO:109

2	106	TNSRPPCVIL	16.000
---	-----	------------	--------

3	53	IEIESRLGGT	8.000
---	----	------------	-------

4	33	CGFEATYLEL	8.000
---	----	------------	-------

5	17	VEPGSGVRI	8.000
---	----	-----------	-------

HLA-B61

1	15	EEVEPGSGV	80.000
---	----	-----------	--------

2	35	FEATYLELA	40.000
---	----	-----------	--------

example of improved peptide **FEATYLELV** **160.000** **enhance P9** SEQ ID NO:110

3	3	GEPGQTSVA	22.000
---	---	-----------	--------

4	65	FEIEINGQL	16.000
---	----	-----------	--------

5	85	YEKDLIEAI	16.000
---	----	-----------	--------

HLA-B61 (10-mer peptides)

1	65	FEIEINGQLV	80.000
---	----	------------	--------

2	17	VEPGSGVRI	40.000
---	----	-----------	--------

3	55	IESRLGGTGA	20.000
---	----	------------	--------

4	87	KDLIEAIRRA	10.000
---	----	------------	--------

example of improved peptide **KELIEAIRRV** **160.000** **enhance P2, P10** SEQ ID NO:111

5	53	IEIESRLGGT	8.000
---	----	------------	-------

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-B62

1	77	KLENGGF ^P Y	24.000	
2	21	SGVRIVV ^E Y	4.800	
3	75	FSKLENGGF	3.000	
4	31	EPCGFEAT ^Y	2.640	<i>P</i> is deleterious @ P2
example of improved peptide		EQCGFEAT ^Y	105.6	replace P with Q @ P2
5	88	DLIEAIRRA	2.200	

HLA-B62 (10-mer peptides)

1	41	ELASAVKEQ ^Y	40.000	
2	58	RLGGTGAF ^E I	9.600	
3	66	EIEINGQLVF	7.920	
4	56	ESRLGGTGAF	6.000	<i>S</i> is deleterious @ P2
example of improved peptide		EQRLGGTGAF	480.000	replace S with Q @ P2
5	20	GSGVRIVV ^E Y	4.800	<i>S</i> is deleterious @ P2
example of improved peptide		GQGVRIVV ^E Y	384.000	replace S with Q @P2

HLA-B7

1	107	NSRPPCVIL	60.000	
example of improved peptide		NPRPPCVIL	1200.000	enhance P2
2	45	AVKEQYP ^G I	6.000	
3	22	GVRIVV ^E Y ^C	5.000	
4	70	NGQLVFSKL	4.000	
5	81	GGFPY ^E KDL	4.000	

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-B7 (10-mer peptides)

1	50	YPGIEIESRL	80.000
2	31	EPCGFEATYL	80.000
3	18	EPGSGVRIVV	6.000

example of improved peptide EPGSGVRLIVL **120.000** **enhance P10**

4	106	TNSRPPCVIL	6.000
5	80	NGGFPYEKDL	4.000

SEQ ID NO:116

HLA-B8

1	107	NSRPPCVIL	4.000
2	45	AVKEQYPGI	1.500
3	105	ITNSRPPCV	0.600
4	56	ESRLGGTGA	0.400
5	100	ETLEKITNS	0.300

S is deleterious @ P9

example of improved peptide ETLEKITNL **12.000** **replace S with L @ P9**

SEQ ID NO:117

HLA-B8 (8-mer peptides)

1	83	FPYEKDLI	6.000
2	107	NSRPPCVI	1.000
3	91	EAIRRASN	0.800

N is deleterious @ P8

example of improved peptide EAIRRASL **32.000** **replace N with L @ P9**

SEQ ID NO:118

4	20	GSGVRIVV	0.600
5	18	EPGSGVRI	0.400

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-B8 (10-mer peptides)

1	50	YPGIEIESRL	0.800
2	93	IRRASNGETL	0.400

example of improved peptide **IA RASNGETL 16.000** **replace R with A @ P2** SEQ ID NO:119

3	31	EPCGFEATYL	0.320
4	104	KITNSRPPCV	0.300
5	18	EPGSGVRIVV	0.240

HLA-B*2702

1	57	SRLGGTGAF	200.000
2	94	RRASNGETL	180.000

example of improved peptide **RRASNGETF 600.000** **enhance P9** SEQ ID NO:120

3	93	IRRASNGET	20.000
4	27	VEYCEPCGF	15.000
5	77	KLENGGFY	9.000

HLA-B*2702 (10-mer peptides)

1	93	IRRASNGETL	60.000
2	94	RRASNGETLE	6.000
3	30	CEPCGFEATY	3.000
4	58	RLGGTGAFEI	2.700
5	23	VRIVVEYCEP	2.000

P is deleterious @ P10

example of improved peptide **VRIVVEYCEY 200.000** **replace P with Y @ P10** SEQ ID NO:121

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-B*2705

1	94	RRASNGETL	6000.000
2	57	SRLGGTGAF	1000.000
3	93	IRRASNGET	200.000

example of improved peptide **IRRASNGEL** **2000.000** **enhance P9** SEQ ID NO:122

4	27	VEYCEPCGF	75.000
5	77	KLENGGFPY	45.000

HLA-B*2705 (10-mer peptides)

1	93	IRRASNGETL	2000.000	
2	94	RRASNGETLE	60.000	<i>E</i> is deleterious @ P2

example of improved peptide **RRASNGETLL** **6000.000** **replace E with L @ P2** SEQ ID NO:123

3	78	LENGGF PYEK	30.000
4	95	RASNGETLEK	30.000
5	58	RLGGTGAFEI	27.000

HLA-B*3501

1	31	EPCGFEATY	40.000
2	75	FSKLENGGF	22.500

example of improved peptide **FPKLENGGM** **120.000** **enhance P2, P9** SEQ ID NO:124

3	107	NSRPPCVIL	15.000
4	42	LASAVKEQY	6.000
5	18	EPGSGVRI	4.000

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-B*3501 (10-mer peptides)

1	31	EPCGFEATYL	30.000
2	50	YPGIEIESRL	20.000
3	56	ESRLGGTGAF	15.000
4	20	GSGVRIVVVEY	10.000
5	83	FPYEKDLIEA	6.000

example of improved peptide **FPYEKDLIEM** **120.000** **enhance P10** SEQ ID NO:125

HLA-B*3701

1	65	FEIEINGQL	15.000
---	----	-----------	--------

example of improved peptide **FDIEINGQL** **60.000** **enhance P2** SEQ ID NO:126

2	47	KEQYPGIEI	10.000
3	85	YEKDLIEAI	10.000
4	17	VEPGSGVRI	10.000
5	35	FEATYLELA	5.000

HLA-B*3701 (10-mer peptides)

1	65	FEIEINGQLV	10.000
---	----	------------	--------

example of improved peptide **FDIEINGQLI** **200.000** **enhance P2, P10** SEQ ID NO:127

2	67	IEINGQLVFS	5.000
3	81	GGFPYEKDLI	5.000
4	87	KDLIEAIRRA	4.000
5	30	CEPCGFEATY	2.000

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-B*3801

1	34	GFEATYLEL	6.000
---	----	-----------	-------

example of improved peptide **GHEATYLEL** **90.000** **enhance P2** SEQ ID NO:128

2	70	NGQLVFSKL	1.560
---	----	-----------	-------

3	38	TYLELASAV	1.040
---	----	-----------	-------

4	81	GGFPYEKDL	1.000
---	----	-----------	-------

5	97	SNGETLEKI	0.720
---	----	-----------	-------

HLA-B*3801 (10-mer peptides)

1	64	AFEIEINGQL	7.800
---	----	------------	-------

example of improved peptide **AHEIEINGQL** **117.000** **enhance P2** SEQ ID NO:129

2	31	EPCGFEATYL	4.800
---	----	------------	-------

3	66	EIEINGQLVF	3.000
---	----	------------	-------

4	26	VVEYCEPCGF	3.000
---	----	------------	-------

5	50	YPGIEIESRL	2.600
---	----	------------	-------

HLA-B*3901

1	94	RRASNGETL	15.000
---	----	-----------	--------

example of improved peptide **RHASNGETL** **90.000** **enhance P2** SEQ ID NO:130

2	34	GFEATYLEL	9.000
---	----	-----------	-------

3	38	TYLELASAV	4.000
---	----	-----------	-------

4	66	EIEINGQLV	3.000
---	----	-----------	-------

5	2	SGEPGQTSV	3.000
---	---	-----------	-------

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-B*3901 (10-mer peptides)

1	33	CGFEATYLEL	12.000
---	----	------------	--------

example of improved peptide **CHFEATYLEL** **360.000** **enhance P2** SEQ ID NO:131

2	64	AFEIEINGQL	9.000
---	----	------------	-------

3	93	IRRASNGETL	4.500
---	----	------------	-------

4	46	VKEQYPGIEI	3.000
---	----	------------	-------

5	16	EVEPGSGVRI	3.000
---	----	------------	-------

HLA-B*3902

1	70	NGQLVFSKL	2.400
---	----	-----------	-------

example of improved peptide **NKQLVFSKL** **24.000** **enhance P2** SEQ ID NO:132

2	81	GGFPYEKDL	2.400
---	----	-----------	-------

3	94	RRASNGETL	2.000
---	----	-----------	-------

4	34	GFEATYLEL	2.000
---	----	-----------	-------

5	107	NSRPPCVIL	0.600
---	-----	-----------	-------

HLA-B*3902 (10-mer peptides)

1	69	INGQLVFSKL	2.400
---	----	------------	-------

2	64	AFEIEINGQL	2.400
---	----	------------	-------

3	50	YPGIEIESRL	2.400
---	----	------------	-------

4	80	NGGFPYEKDL	2.400
---	----	------------	-------

5	106	TNSRPPCVIL	2.000
---	-----	------------	-------

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-B*4403

1	67	IEINGQLVF	200.000
---	----	-----------	---------

example of improved peptide IEINGQLVY **900.000** **enhance P9** SEQ ID NO:133

2	27	VEYCEPCGF	40.000
---	----	-----------	--------

3	21	SGVRIVVEY	36.000
---	----	-----------	--------

4	65	FEIEINGQL	20.000
---	----	-----------	--------

5	35	FEATYLELA	12.000
---	----	-----------	--------

HLA-B*4403 (10-mer peptides)

1	30	CEPCGFEATY	120.000
---	----	------------	---------

2	53	IEIESRLGGT	30.000
---	----	------------	--------

example of improved peptide IEIESRLGGY **900.000** **enhance P10** SEQ ID NO:134

3	67	IEINGQLVFS	30.000
---	----	------------	--------

4	65	FEIEINGQLV	20.000
---	----	------------	--------

5	17	VEPGSGVRIV	18.000
---	----	------------	--------

HLA-B*5101

1	18	EPGSGVRIV	484.000
---	----	-----------	---------

2	59	LGGTGAFEI	114.400
---	----	-----------	---------

example of improved peptide LPGTGAFEI **572.000** **enhance P2** SEQ ID NO:135

3	2	SGEPGQTSV	48.400
---	---	-----------	--------

4	81	GGFPYEKDL	44.000
---	----	-----------	--------

5	70	NGQLVFSKL	22.000
---	----	-----------	--------

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-B*5101 (10-mer peptides)

1	18	EPGSGVRIVV	440.000
2	44	SAVKEQYPGI	220.000

example of improved peptide	SPVKEQYPGI	440.000	enhance P2	SEQ ID NO:136
3	31	EPCGFEATYL	220.000	
4	81	GGFPYEKDLI	176.000	
5	50	YPGIEIESRL	157.300	

HLA-B*5102

1	18	EPGSGVRIV	242.000
2	81	GGFPYEKDL	110.000

example of improved peptide	GPFPYEKDI	2200.000	enhance P2, P9	SEQ ID NO:137
3	59	LGGTGAFEI	96.800	
4	70	NGQLVFSKL	48.400	
5	2	SGEPGQTSV	24.200	

HLA-B*5102 (10-mer peptide)

1	44	SAVKEQYPGI	726.000
---	----	------------	---------

example of improved peptide	SPVKEQYPGI	1452.000	enhance P2	SEQ ID NO:138
2	50	YPGIEIESRL	400.000	
3	81	GGFPYEKDLI	400.000	
4	18	EPGSGVRIVV	220.000	
5	31	EPCGFEATYL	121.000	

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-B*5103

1	59	LGGTGAFEI	48.400
---	----	-----------	--------

example of improved peptide LAFTGAFEI **145.200** enhance P2 SEQ ID NO:139

2	2	SGEPGQTSV	44.000
---	---	-----------	--------

3	18	EPGSGVRIV	44.000
---	----	-----------	--------

4	70	NGQLVFSKL	7.260
---	----	-----------	-------

5	81	GGFPYEKDL	7.200
---	----	-----------	-------

HLA-B*5103 (10-mer peptide)

1	44	SAVKEQYPGI	110.000
---	----	------------	---------

2	81	GGFPYEKDLI	52.800
---	----	------------	--------

3	18	EPGSGVRIVV	44.000
---	----	------------	--------

example of improved peptide EAGSGVRIVV **110.000** enhance P2 SEQ ID NO:140

4	60	GGTGAFIEI	44.000
---	----	-----------	--------

5	33	CGFEATYLEL	7.920
---	----	------------	-------

HLA-B*5201

1	18	WPGSGVRIV	75.000
---	----	-----------	--------

2	67	LEINGQLVF	22.500
---	----	-----------	--------

example of improved peptide LQINGQLVI **450.000** enhance P2, P9 SEQ ID NO:141

3	59	LGGTGAFEI	11.250
---	----	-----------	--------

4	98	NGETLEKIT	11.000
---	----	-----------	--------

5	19	PGSGVRIVV	10.000
---	----	-----------	--------

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-B*5201 (10-mer peptides)

1	18	EPGSGVRIVV	100.000
2	17	VEPGSGVRIV	45.000

example of improved peptide **VQPGSGVRIV 450.000** **enhance P2** SEQ ID NO:142

3	81	GGFPYEKDLI	33.000
4	105	ITNSRPPCVI	15.000
5	37	ATYPELASAV	12.000

HLA-B*5801

1	75	FSKLENGGF	40.000
---	----	-----------	--------

example of improved peptide **FSKLENGGW 80.000** **enhance P9** SEQ ID NO:143

2	42	LASAVKEQY	4.500
3	107	NSRPPCVIL	4.000
4	61	GTGAFEIEI	3.000
5	105	ITNSRPPCV	3.000

HLA-B*5801 (10-mer peptides)

1	56	ESRLGGTGAF	12.000
2	20	GSGVRIVVVEY	10.800

example of improved peptide **GSGVRIVVVEW 144.000** **enhance P10** SEQ ID NO:144

3	1	MSGEPGQTSV	4.000
4	105	ITNSRPPCVI	3.000
5	37	ATYPELASAV	3.000

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

HLA-Cw*0301

1	65	FEIEINGQL	30.000
2	81	GGFPYEKDL	18.000
3	70	NGQLVFSKL	12.000
4	57	SRLGGTGAF	10.000
5	34	GFEATYLEL	10.000

HLA-Cw*0301 (10-mer peptides)

1	44	SAVKEQYPGI	50.000
---	----	------------	--------

example of improved peptide		SAVKEQYPGL	100.000	enhance P10	SEQ ID NO:145
2	33	CGFEATYLEL	45.000		
3	69	INGQLVFSKL	12.000		
4	81	GGFPYEKDLI	3.750		
5	106	TNSRPPCVIL	3.000		

HLA-Cw*0401

1	34	GFEATYLEL	240.000
2	38	TYLELASAV	30.000
3	82	GFPYEKDLI	25.000
4	18	EPGSGVRI	20.000
5	31	EPCGFEATY	12.000

example of improved peptide		EFCGFEATL	200.000	enhance P2, P9	SEQ ID NO:146
--------------------------------	--	-----------	----------------	-----------------------	---------------

HLA-Cw*0401 (10-mer peptides)

1	64	AFEIEINGQL	200.000
2	74	VFSKLENGGF	100.000

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
------	----------------	-------------	--	------------

example of improved peptide		VFSKLENGGL	200.000	enhance P10	SEQ ID NO:147
3	50	YPGIEIESRL	80.000		
4	31	EPCGFEATYL	80.000		
5	18	EPGSGVRIVV	10.000		

HLA-Cw*0602

1	85	YEKDLIEAI	6.600
2	65	FEIEINGQL	6.600
3	21	SGVRIVVEY	6.000
4	31	EPCGFEATY	3.300
5	61	GTGAGEIEI	3.000

HLA-Cw*0702

1	31	EPCGFEATY	24.000
2	21	SGVRIVVEY	19.200
3	42	LASAVKEQY	8.800
4	77	KLENGGFPY	4.000
5	49	QYPGIEIES	2.880

HLA-Cw*0702 (10-mer peptides)

1	20	GSGVRIVVEY	38.400
2	30	CEPCGFEATY	16.000
3	41	ELASAVKEQY	16.000
4	50	YPGIEIESRL	7.920
5	76	SKLENGGFPY	4.000